

0400 #3



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## RAW SEQUENCE LISTING

DATE: 02/07/2002

PATENT APPLICATION: US/10/046,649

TIME: 11:08:26

Input Set : N:\Crf3\RULE60\10046649.raw

Output Set: N:\CRF3\02072002\J046649.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Young, Richard S.

7 (ii) TITLE OF INVENTION: Stress Proteins and Uses Therefor

9 (iii) NUMBER OF SEQUENCES: 4

11 (iv) CORRESPONDENCE ADDRESS:

12 (A) ADDRESSEE: Hamilton, Brook, Smith &amp; Reynolds, P.C.

13 (B) STREET: 2 Militia Drive

14 (C) CITY: Lexington

15 (D) STATE: MA

16 (E) COUNTRY: USA

17 (F) ZIP: 02173

19 (v) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: Floppy disk

21 (B) COMPUTER: IBM PC compatible

22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

25 (vi) CURRENT APPLICATION DATA:

C--&gt; 26 (A) APPLICATION NUMBER: US/10/046,649

C--&gt; 27 (B) FILING DATE: 14-Jan-2002

38 (C) CLASSIFICATION: 435

C--&gt; 53 (vii) PRIOR APPLICATION DATA:

31 (A) APPLICATION NUMBER: 08/336,251

32 (B) FILING DATE:

36 (A) APPLICATION NUMBER: US 08/073,381

37 (B) FILING DATE: 04-JUN-1993

42 (A) APPLICATION NUMBER: US 07/804,632

43 (B) FILING DATE: 09-DEC-1991

46 (A) APPLICATION NUMBER: US 07/366,581

47 (B) FILING DATE: 15-JUN-1989

50 (A) APPLICATION NUMBER: US 07/207,298

51 (B) FILING DATE: 15-JUN-1988

54 (A) APPLICATION NUMBER: PCT/US89/02619

55 (B) FILING DATE: 15-JUN-1989

C--&gt; 57 (viii) ATTORNEY/AGENT INFORMATION:

58 (A) NAME: Granahan, Patricia

59 (B) REGISTRATION NUMBER: 32,227

60 (C) REFERENCE/DOCKET NUMBER: WHI88-08AFA3

C--&gt; 62 (ix) TELECOMMUNICATION INFORMATION:

63 (A) TELEPHONE: (617) 861-6240

66 (2) INFORMATION FOR SEQ ID NO: 1:

68 (i) SEQUENCE CHARACTERISTICS:

69 (A) LENGTH: 573 amino acids

ENTERED

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```

70      (B) TYPE: amino acid
71      (D) TOPOLOGY: linear
72      (ii) MOLECULE TYPE: protein
73      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
74      Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg
75      1          5          10          15
76      Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe
77      20          25          30
78      Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala
79      35          40          45
80      Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile
81      50          55          60
82      Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val
83      65          70          75          80
84      Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys
85      85          90          95
86      Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly
87      100          105          110
88      Thr Thr Thr Ala Thr Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe
89      115          120          125
90      Glu Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val
91      130          135          140
92      Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys
93      145          150          155          160
94      Pro Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala
95      165          170          175
96      Asn Gly Asp Lys Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys
97      180          185          190
98      Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn
99      195          200          205
100     Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile
101     210          215          220
102     Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln
103     225          230          235          240
104     Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln Ser
105     245          250          255
106     Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro Leu Val
107     260          265          270
108     Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Val Leu
109     275          280          285
110     Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro Gly
111     290          295          300
112     Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile Ala Thr
113     305          310          315          320
114     Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Thr Leu Asn Leu Glu Asp
115     325          330          335
116     Val Gln Pro His Asp Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys
117     340          345          350
118     Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp Lys Ala Gln Ile Glu

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RAW SEQUENCE LISTING  
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```

149          355          360          365
151  Lys Arg Ile Gln Glu Ile Ile Glu Gln Leu Asp Val Thr Thr Ser Glu
152          370          375          380
154  Tyr Glu Lys Glu Lys Leu Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly
155          385          390          395          400
157  Val Ala Val Leu Lys Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu
158          405          410          415
160  Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val
161          420          425          430
163  Glu Glu Gly Ile Val Leu Gly Gly Cys Ala Leu Leu Arg Cys Ile
164          435          440          445
166  Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly
167          450          455          460
169  Ile Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala
170          465          470          475          480
172  Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met Gln
173          485          490          495
175  Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe Val Asn
176          500          505          510
178  Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala
179          515          520          525
181  Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu Val
182          530          535          540
184  Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met Gly Ala
185          545          550          555          560
187  Met Gly Gly Met Gly Gly Gly Met Gly Gly Met Phe
188          565          570

```

190 (2) INFORMATION FOR SEQ ID NO: 2:

192 (i) SEQUENCE CHARACTERISTICS:

193 (A) LENGTH: 547 amino acids

194 (B) TYPE: amino acid

195 (D) TOPOLOGY: linear

197 (ii) MOLECULE TYPE: protein

201 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

203  Met Ala Ala Lys Asp Val Lys Phe Gly Asn Asp Ala Arg Val Lys Met
204  1          5          10          15
207  Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys Val Thr Leu Gly
208          20          25          30
210  Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr
211          35          40          45
213  Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Pro Glu Asp
214          50          55          60
216  Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
217          65          70          75          80
219  Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
220          85          90          95
223  Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn
224          100          105          110
226  Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Thr Ala Ala Val

```

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227																	
229	Glu	Glu	Leu	Lys	Ala	Leu	Ser	Val	Pro	Cys	Ser	Asp	Ser	Lys	Ala	Ile	
230		130					135					140					
232	Ala	Gln	Val	Gly	Thr	Ile	Ser	Ala	Asn	Ser	Asp	Glu	Thr	Val	Gly	Lys	
233	145					150					155					160	
235	Leu	Ile	Ala	Glu	Ala	Met	Asp	Lys	Val	Gly	Lys	Glu	Gly	Val	Ile	Thr	
236					165					170						175	
238	Val	Glu	Asp	Gly	Thr	Gly	Leu	Gln	Asp	Glu	Leu	Asp	Val	Val	Glu	Gly	
239				180					185					190			
241	Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro	Tyr	Phe	Ile	Asn	Lys	Pro	
242		195						200					205				
244	Glu	Thr	Gly	Ala	Val	Glu	Leu	Glu	Ser	Pro	Phe	Ile	Leu	Leu	Ala	Asp	
245	210					215						220					
248	Lys	Lys	Ile	Ser	Asn	Ile	Arg	Glu	Met	Leu	Pro	Val	Leu	Glu	Ala	Val	
249	225					230					235					240	
251	Ala	Lys	Ala	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	
252				245						250					255		
254	Glu	Ala	Leu	Ala	Thr	Ala	Val	Val	Asn	Thr	Ile	Arg	Gly	Ile	Val	Lys	
255			260						265					270			
257	Val	Ala	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Met	
258		275						280					285				
260	Leu	Gln	Asp	Ile	Ala	Thr	Leu	Thr	Gly	Gly	Thr	Val	Ile	Ser	Glu	Glu	
261	290					295						300					
263	Ile	Gly	Met	Glu	Leu	Glu	Lys	Ala	Thr	Leu	Glu	Asp	Leu	Gly	Gln	Ala	
264	305					310					315					320	
266	Lys	Arg	Val	Val	Ile	Asn	Lys	Asp	Thr	Thr	Thr	Ile	Ile	Asp	Gly	Val	
267				325						330					335		
269	Gly	Glu	Glu	Ala	Ala	Ile	Gln	Gly	Arg	Val	Ala	Gln	Ile	Arg	Gln	Gln	
270			340					345					350				
272	Ile	Glu	Glu	Ala	Thr	Ser	Asp	Tyr	Asp	Arg	Glu	Lys	Leu	Gln	Glu	Arg	
273		355					360						365				
275	Val	Ala	Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Ala	
276	370					375					380						
278	Thr	Glu	Val	Glu	Met	Lys	Glu	Lys	Lys	Ala	Arg	Val	Glu	Asp	Ala	Leu	
279	385				390						395					400	
281	His	Ala	Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	Val	Val	Ala	Gly	Gly	Gly	
282				405						410					415		
284	Val	Ala	Leu	Ile	Arg	Val	Ala	Ser	Lys	Leu	Ala	Asp	Leu	Arg	Gly	Gln	
285			420						425				430				

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```

302 Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu Pro Lys Asn Asp Ala
303      515      520      525
305 Ala Asp Leu Gly Ala Ala Gly Gly Met Gly Gly Met Gly Gly Met Gly
306      530      535      540
308 Gly Met Met
309      545
311 (2) INFORMATION FOR SEQ ID NO: 3:
313 (i) SEQUENCE CHARACTERISTICS:
314 (A) LENGTH: 540 amino acids
315 (B) TYPE: amino acid
316 (D) TOPOLOGY: linear
318 (ii) MOLECULE TYPE: protein
322 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
324 Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg Arg Gly Leu Glu
325 1      5      10      15
327 Arg Gly Leu Asn Ser Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro
328      20      25      30
331 Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala Pro Thr Ile
332      35      40      45
334 Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu Leu Glu Asp Pro
335      50      55      60
337 Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu Val Ala Lys Lys Thr
338      65      70      75      80
340 Asp Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln
341      85      90      95
343 Ala Leu Val Lys Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro
344      100      105      110
346 Leu Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Asp Lys Val Thr Glu
347      115      120      125
350 Thr Leu Leu Lys Asp Ala Lys Glu Val Glu Thr Lys Glu Gln Ile Ala
351      130      135      140
353 Ala Thr Ala Ala Ile Ser Ala Gly Asp Gln Ser Ile Gly Asp Leu Ile
354      145      150      155      160
356 Ala Glu Ala Met Asp Lys Val Gly Asn Glu Gly Val Ile Thr Val Glu
357      165      170      175
359 Glu Ser Asn Thr Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg
360      180      185      190
362 Phe Asp Lys Gly Tyr Ile Ser Gly Tyr Phe Val Thr Asp Ala Glu Arg
363      195      200      205
365 Gln Glu Ala Val Leu Glu Glu Pro Tyr Ile Leu Leu Val Ser Ser Lys
366      210      215      220
368 Val Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gln
369      225      230      235      240
372 Ala Gly Lys Ser Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Ala
373      245      250      255
375 Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr Phe Lys Ser Val
376      260      265      270
378 Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Gln
379      275      280      285

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/046,649

DATE: 02/07/2002

TIME: 11:08:27

Input Set : N:\Crf3\RULE60\10046649.raw

Output Set: N:\CRF3\02072002\J046649.raw

L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:35 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:41 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:45 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:49 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:53 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:57 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]  
L:62 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]